

G. SEQUENCE LISTING

5 (1) GENERAL INFORMATION

(i) **APPLICANT:** Darrell Anderson, Nabil Hanna, John Leonard,
Roland Newman and Mitchell Reff and William H.
Rastetter

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(ii) **TITLE OF INVENTION:** THERAPEUTIC APPLICATION OF
CHIMERIC AND RADIOLABELED
ANTIBODIES TO HUMAN B
LYMPHOCYTE RESTRICTED
15 DIFFERENTIATION ANTIGEN FOR
TREATMENT OF B CELL LYMPHOMA

(iii) **NUMBER OF SEQUENCES:** 8

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(iv) **CORRESPONDING ADDRESS:**

(A) **ADDRESSEE:** IDEC Pharmaceuticals Corporation
(B) **STREET:** 11011 Torreyana Road
(C) **CITY:** San Diego
(D) **STATE:** California
(E) **COUNTRY:** USA
(F) **ZIP:** 92121

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sh
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(v) **COMPUTER READABLE FORM:**

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(A) **MEDIUM TYPE:** Diskette, 3.5 inch, 1.44 Mb
(B) **COMPUTER:** Macintosh
(C) **OPERATING SYSTEM:** MS.DOS
(D) **SOFTWARE:** Microsoft Word 5.0

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(vi) **CURRENT APPLICATION DATA:**

(A) **APPLICATION NUMBER:**
(B) **FILING DATE:**
(C) **CLASSIFICATION:**

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(viii) **ATTORNEY/AGENT INFORMATION:**

(A) **NAME:** Burgoon, Richard P. Jr.
(B) **REGISTRATION NUMBER:** 34,787
(C) **REFERENCE/DOCKET NUMBER:**

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(ix) **TELECOMMUNICATION INFORMATION:**

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(A) **TELEPHONE:** (619) 550-8500
(B) **TELEFAX:** (619) 550-8750

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8540 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: ^{NO}yes

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
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CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
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CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1140
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 5 TGTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC 1440
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 15 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740
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 20 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860
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 10 CAGCCAGTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CAGTGTACA GAGTTCTTGA 7200
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 35 CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAGCG GTTAGCTCCT 7980
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 50 GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
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 55 TTCCCCGAAA AGTGCCACCT 8540

(3) INFORMATION FOR SEQ ID NO: 2:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9209 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

B

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: ^{no} ~~yes~~
(iv) ANTI-SENSE: no
(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

C1

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10	AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC	120
15	GGAGAATGGG CGGAAC ^T TGGG CGGAGTTAGG GGC ^G GGGATGG GCGGAGTTAG GGGCGGGACT	180
20	ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG	240
25	GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT	300
30	GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT	360
35	AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC	420
40	GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG	480
45	ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA	540
50	TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA	600
55	AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCAGTAC	660
60	ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC	720
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	GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA	900
	CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC	960
	CATCACAGAT CTCTCACTAT GGATTTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT	1020
	GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT	1080
	GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTCAAGTGT AAGTTACATC	1140
	CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCCT GGATTTATGC CACATCCAAC	1200
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	TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG	1440

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5 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
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 10 ~~CTGACGAAGA ASCAGCTCA~~ ~~CCTGACCTGC~~ ~~GTGCTCAAA~~ ~~GETTCTATCC~~ ~~CAGCAGACATG~~ 3600
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 ATAGAGAGGG CAGGAGCCAG GGCAGASCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500
 40 CATTTGCTTC TGACATAGTT GTGTTGGGAG CTTGGATAGC TTGGACAGCT CAGGGCTGCG 4560
 ATTTGCGGCC AAACCTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620
 45 GCCATCATGG TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680
 AAGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
 ACCACAACCT CTTCACTGGA AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800
 50 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
 GAACTCAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGA TGATGCCTTA 4920
 55 AGACTTATTG AACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980
 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
 ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCAGAAA TTGATTGGG GAAATATAAA 5100
 60 CTTCTCCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160
 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220

CTCCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA GATCAGCCTC 5280
 GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC TCCCCCGTGC CTTCTTGAC 5340
 5 CCTGGAAGGT GCCACTCCCA CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCATTG 5400
 TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
 10 TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TGGGGTGGGC TCTATGGAAC CAGCTGGGGC 5520
 TCGAGCTACT AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 5580
 AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
 15 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 5700
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCAGAA 5760
 20 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880
 CTGACATAGT TGTGTTGGA GCTTGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
 25 CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTCGGC TATGACTGGG CACAACAGAC 6000
 AATCGGCTGC TCTGATGCCG CCGTGTTCCG GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT 6060
 30 TGTCAGACC GACCTGTCCG GTGCCCTGAA TGAAGTGCAG GACGAGGCAG CGCGGCTATC 6120
 GTGGCTGGCC ACGACGGGCG TTCCTTGCGC AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
 AAGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTCAT CTCACCTTGC 6240
 35 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC 6300
 GGCTACCTGC CCATTGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
 40 GGAAGCCGGT CTTGTGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
 CGAACTGTTC GCCAGGCTCA AGGCGCGCAT GCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
 TGGCGATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTTCTG GATTCATCGA 6540
 45 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT 6600
 TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GTATCGCCGC 6660
 50 TCCCGATTCT CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCT GAGCGGGACT 6720
 CTGGGGTTCT AAATGACCGA CCAAGCGACG CCCAACCTGC CATCACGAGA TTTCGATTCC 6780
 ACCGCCGCCT TCTATGAAAG GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840
 55 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCCC ACCCCAATT GTTTATTGCA 6900
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTT 6960
 60 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
 GCGGCCGCGA TCCCGTCGAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
 ATTGTTATCC GCTCACAATT CCACACAACA TAGGAGCCGG AAGCATAAAG TGTAAAGCCT 7140

5 GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 7200
 AGTCGGGAAA CCTGTCTGTC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 7260
 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCTGTC 7320
 10 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA 7440
 AGGCCGCGTT GCTGCGGTTT TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC 7500
 15 GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC 7560
 CTGGAAGCTC CCTCGTGGCG TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
 20 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCAGC 7740
 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 25 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTTGAA GTGGTGGCTT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAACAAA 7980
 30 CCACCGCTGG TAGCGGTGGT TTTTGTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT 8100
 35 CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA 8160
 ATTAAAAATG AAGTTTAAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT 8220
 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG 8280
 40 TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC 8400
 45 AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG 8520
 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA 8580
 50 GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
 TTAGCTCCTT CGGTCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGAGTG TTATCACTCA 8700
 55 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG 8760
 TGA CTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT 8820
 CTTGCCCCGG GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
 60 TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
 GTTCGATGTA ACCCACTCGT GCACCCAAC TATCTTCAGC ATCTTTTACT TTCACCAGCG 9000

TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
 GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 5 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT 9209

10 (4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 54 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: ^{no}yes

(iv) ANTI-SENSE: no

25 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

5' ATC ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT
 TC 3'

52
 542
 1

30

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 30 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: ^{no}yes

(iv) ANTI-SENSE: yes

45

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3'

30

50

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 384 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: ^{no}~~yes~~

10

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

15 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC 51
ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT 102
20 GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA 153
AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG 204
ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC 255
25 AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA 306
GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG ACT AGT AAC CCA CCC ACG TTC 357
30 GGA GGG GGG ACC AAG CTG GAA ATC AAA 384

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 27 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: ^{no}~~yes~~

45

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50

5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3'

27

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 29 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: ^{no}yes

(iv) ANTI-SENSE: yes

15 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5' GGS TGT TGT GCT AGC TGM RGA GAC RGT GA 3' 29

20 (9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 420 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: ^{no}yes

(iv) ANTI-SENSE: no

35 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

40 ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC 51
CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG 102
GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC 153
45 AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA 204
GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC 255
AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC 306
50 AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA AGA TCG ACT 357
TAC TAC GGC GGT GAC TCG TAC TTC AAT GTC TGG GGC GCA GGG ACC ACG GTC 408
ACC GTC TCT GCA 420